SEQUENCE LISTING

<110> Ago, Hideo
      Miyano, Masashi
      Adachi, Tsuyoshi

<120> HCV Polymerase Suitable for Crystal
  Structure Analysis and Method for Using the Enzyme

<130> SHIM007

<140> 09/608,713
<141> 2000-06-30

<150> 11-188630
<151> 1999-07-02

<150> 11-192488
<151> 1999-07-07

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1
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<212> PRT
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His His Asn Met Val Tyr Ala Thr Thr Ser Arg Ser Ala Gly Leu Arg
         35   40   45
Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His Tyr
     50   55   60
Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val Lys Ala
65   70   75   80
Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro His Ser
                 85   90   95
Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu Ser
             100   105   110
Ser Lys Ala Val Asn His Ile His Ser Val Trp Lys Asp Leu Leu Glu
             115   120   125

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Phe Cys Val Gln Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu Ile
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Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr
                165               170               175
Asp Val Val Ser Thr Leu Pro Gln Val Val Met Gly Ser Ser Tyr Gly
            180               185               190
Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn Thr Trp
        195               200               205
Lys Ser Lys Lys Asn Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe
    210               215               220
Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr
225               230               235               240
Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu
            245               250               255
Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln
            260               265               270
Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser
        275               280               285
Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg
        290               295               300
Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp Leu
305               310               315               320
Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu
            325               330               335
Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp
            340               345               350
Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser
        355               360               365
Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr Leu
    370               375               380
Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr Ala
385               390               395               400
Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr Ala
                405               410               415
Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser Ile
            420               425               430
Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile Tyr
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Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile Glu
    450               455               460
Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro Gly
465               470               475               480
Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro Pro
            485               490               495
Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu Leu
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Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn Trp
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Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser Gln
        530                 535                 540
Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp Ile
545                 550                 555                 560
Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Trp Phe Met Leu Cys Leu
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      C-terminus

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1031, 1095, 1183, 1149, 1270, 1349, 1405, 1408, 1501, 1588,
1604, 1679, 1824, 1899, 2076, 2086, 2221, 2225, 2240, 2313,
2445, 2605, 2634, 2760
<223> n = A,T,C or G

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<223> DNA encoding fusion protein consisting of a
      portion of HCV polymerase and histidine tag at the
      C-terminus

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1604, 1679, 1824, 1899, 2076, 2086, 2221, 2225, 2240, 2313,
2445, 2605, 2634, 2760
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1604, 1679, 1824, 1899, 2076, 2086, 2121, 2225, 2240, 2313,
2445, 2605, 2634, 2760
<223> n = A,T,C or G


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Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala
 1               5                  10                  15


mts rmt srt yrt hrt rth rgy aau thr rcy saa gcg gag gaa agc aag     96
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Ala Glu Glu Ser Lys
                20                  25                  30


ctg ccc atc aac gcg ttg agc aac tct ttg ctg aag ugu sry sur asn    144
Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu Lys Cys Xaa Xaa Xaa
            35                  40                  45


aau sra sns ruu cgc cac cat aac atg gtt tat gcc aca aca tct cgc    192
Asn Xaa Xaa Xaa Arg His His Asn Met Val Tyr Ala Thr Thr Ser Arg
        50                  55                  60


agc gca ggc ctg arg hsh sas nmt vat yra ath rth rsr arg sra agy    240
Ser Ala Gly Leu Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa
 65                  70                  75                  80


ucg gca gaa gaa ggt cac ctt tga cag act gca agt cct gga cga cca    288
Ser Ala Glu Glu Gly His Leu  *  Gln Thr Ala Ser Pro Gly Arg Pro
                85                  90                  95


car ggn ysy sva thr has arg ugn vau asa shs tac cgg gac gtg ctc    336
Gln Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Arg Asp Val Leu
                100                 105                 110


aag gag atg aag gcg aag gcg tcc aca gtt aag tyr arg asv auy sgu    384
Lys Glu Met Lys Ala Lys Ala Ser Thr Val Lys Xaa Xaa Xaa Xaa Xaa
                115                 120                 125


mty saa ysa asr thr vay sgc taa act cct atc cgt aga gga agc ctg    432
Xaa Xaa Xaa Xaa Xaa Xaa Xaa  *  Thr Pro Ile Arg Arg Gly Ser Leu
                130                 135                 140


caa gct gac gcc ccc aca taa ysu usr vag ugu aac ysy sut hrr rhs    480
Gln Ala Asp Ala Pro Thr  *  Xaa Xaa Xaa Cys Asn Xaa Xaa Xaa Xaa
                145                 150                 155


tcg gcc aaa tcc aag ttt ggc tat ggg gca aag gac gtc cgg aac cta    528
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Ser Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu
        160             165                 170


sra ays sry shg yty rgy aay sas vaa rga snu tcc agc aag gcc gtt    576
Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Ser Ser Lys Ala Val
        175             180                 185


aac cac atc cac tcc gtg tgg aag gac ttg ctg srs rys aav aas nhs    624
Asn His Ile His Ser Val Trp Lys Asp Leu Leu Xaa Xaa Xaa Xaa Xaa
190             195                 200                 205


hss rva try sas uug aag aca ctg tga cac caa ttg aca cca cca tca    672
Xaa Xaa Xaa Xaa Leu Lys Thr Leu  *  His Gln Leu Thr Pro Pro Ser
                210                 215                 220


tgg caa aaa atg agg uas thr vat hrr ast hrt hrm taa ysa sng ugt    720
Trp Gln Lys Met Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa  *  Xaa Xaa Xaa
                225                 230                 235


ttt ctg tgt cca acc aga gaa agg agg ccg taa gcc agc ccg cct tva    768
Phe Leu Cys Pro Thr Arg Glu Arg Arg Pro  *  Ala Ser Pro Pro Xaa
                240                 245                 250


hcy sva gnr guy sgy gya rgy sra aar qua tcg tat tcc cag atc tgg    816
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Val Ser Tyr Ser Gln Ile Trp
                255                 260                 265


gag tcc gtg tat gcg aga aga tgg ccc tcv ahr asu gyv aar gva cys    864
Glu Ser Val Tyr Ala Arg Arg Trp Pro Xaa Xaa Xaa Xaa Lys Xaa Xaa
                270                 275                 280


guy smt aau tat gat gtg gtc tcc acc ctt cct cag gtc gtg atg ggc    912
Xaa Xaa Asn Tyr Asp Val Val Ser Thr Leu Pro Gln Val Val Met Gly
                285                 290                 295


tcc tca tac tyr asv ava srt hru rgn vav amt gys rsr tyr gga ttc    960
Ser Ser Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Phe
        300                 305                 310


cag tac tct cct ggg cag cga gtc gag ttc ttg gtg aat acc gyh gnt   1008
Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn Thr Xaa Xaa
315                 320                 325                 330


yrs rrg ygn arg vag uhu vaa snt hrt gga aat caa aga aaa acc cca   1056
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Asn Gln Arg Lys Thr Pro
                335                 340                 345


tgg gct ttt cat atg aca ctc gct gtt rys sry sys asn rmt gyh srt   1104
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Trp Ala Phe His Met Thr Leu Ala Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            350             355             360

yra sth rar gcy stt cga ctc aac ggt cac cga gaa cga cat ccg tgt    1152
Xaa Xaa Xaa Xaa Xaa Arg Leu Asn Gly His Arg Glu Arg His Pro Cys
        365             370             375

tga gga gtc aat tha ssr thr vat hrg nas nas arg vag ugu srt acc    1200
 *  Gly Val Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Thr
        380             385             390

aat gtt gtg act tgg ccc ccg aag cca gac agg cca taa aat cgt yrg    1248
Asn Val Val Thr Trp Pro Pro Lys Pro Asp Arg Pro  *  Asn Arg Xaa
    395             400             405

ncy scy sas uaa rgu aaa rgg naa yss rct cac aga gcg gct tta tat    1296
Xaa Xaa Xaa  *  Xaa Lys Xaa Xaa Xaa Xaa His Arg Ala Ala Leu Tyr
    410             415             420

cgg ggg tcc tct gac taa ttc aaa agg gut hrg uar gut yrg ygy rut    1344
Arg Gly Ser Ser Asp  *  Phe Lys Arg Arg Xaa Xaa Xaa Xaa Xaa Xaa
    425             430             435

hra sns rys gyc aga act gcg gtt atc gcc ggt gcc gcg cga gcg gcg    1392
Xaa Xaa Xaa Xaa Arg Thr Ala Val Ile Ala Gly Ala Ala Arg Ala Ala
    440             445             450

tgc tga cga ctg nas ncy sgy tyr arg arg cys arg aas rgy vau thr    1440
Cys  *  Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
455             460             465

thr agc tgc ggt aac acc ctc aca tgt tac ttg aag gcc tct gca gcc    1488
Xaa Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala
470             475             480             485

tgt src ysg yas nth rut hrc yst yru ysa asr aaa acy scg agc tgc    1536
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Ser Cys
            490             495             500

gaa gct cca gga ctg cac gat gct cgt gaa cgg aga cga car gaa aay    1584
Glu Ala Pro Gly Leu His Asp Ala Arg Glu Arg Arg Arg Gln Glu Asn
            505             510             515

sug nas cys thr mtu vaa sng yas asc tcg tcg tta tct gtg aaa gcg    1632
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ser Leu Ser Val Lys Ala
            520             525             530

cgg gaa ccc aag agg acg cgg cga gcu vav acy sgu sra agy thr gng    1680
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Arg Glu Pro Lys Arg Thr Arg Arg Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    535                 540                 545


uas aaa asr cta cga gtc ttc acg gag gct atg act agg tac tcc gcc      1728
Xaa Lys Xaa Leu Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala
550                 555                 560                 565


ccc ccc ggg uar gva hthrguaamt thrargtyrs raarrgygac ccgccccaac     1783
Pro Pro Gly Xaa Xaa
                570


cagaatacga cttggagctg ataacatcat gttccasrrg nrgutyrasu guuthrsrcy   1843
ssrtccaatg tgtcggtcgc ccacgatgca tcaggcaaaa gggtgtacta csrasnvasr   1903
vaaahsasaa srgyysargv atyrtyrctc accgtgatc ccaccaccc cctcgcacgg    1963
gctgcgtggg agacauthra rgasrthrth rruaaargaa aatrguthrg ctagacacac   2023
tccagttaac tcctggctag gcaacattat tatgtataaa rghsthrrva asnsrtrugy   2083
asnmttyrgc gcccacttg tgggcaagga tgattctgat gactcacttc ttctccaart   2143
hrutraaarg mtumtthrhs hhsratcctt ctagcgcagg agcaacttya aaaagccctg   2203
gactgccaga tcuuaagngu gnuguysaau ascysgntac ggggcctgtt actccattga   2263
gccacttgac ctacctcaga tcatttyrgy aacystyrsr guruasurgn gaacgactcc   2323
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tacagcgggg gagacgnuas usrgytrhva aagytyrsrg ygyasatata tcacagcctg   2803
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<221> VARIANT
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254, 255, 256, 257, 258, 276, 277, 278, 279, 281, 282
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<221> VARIANT
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<223> Xaa = Any Amino Acid

<223> DNA encoding fusion protein consisting of a
      portion of HCV polymerase and histidine tag at the
      C-terminus

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Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Ala Glu Glu Ser Lys
                20                  25                  30
Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu Lys Cys Xaa Xaa Xaa
        35                  40                  45
Asn Xaa Xaa Xaa Arg His His Asn Met Val Tyr Ala Thr Thr Ser Arg
    50                  55                  60
Ser Ala Gly Leu Xaa Xaa Xaa Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa
65                  70                  75                  80
Ser Ala Glu Glu Gly His Leu Gln Thr Ala Ser Pro Gly Arg Pro Gln
                85                  90                  95
Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Arg Asp Val Leu Lys
            100                 105                 110
Glu Met Lys Ala Lys Ala Ser Thr Val Lys Xaa Xaa Xaa Xaa Xaa Xaa
            115                 120                 125
Xaa Xaa Xaa Xaa Xaa Xaa Thr Pro Ile Arg Arg Gly Ser Leu Gln Ala
    130                 135                 140
Asp Ala Pro Thr Xaa Xaa Xaa Cys Asn Xaa Xaa Xaa Xaa Ser Ala Lys
145                 150                 155                 160
Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu Xaa Xaa Xaa
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                     165                        170                        175
Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Ser Ser Lys Ala Val Asn His Ile
            180                    185                    190
His Ser Val Trp Lys Asp Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        195                    200                    205
Xaa Leu Lys Thr Leu His Gln Leu Thr Pro Pro Ser Trp Gln Lys Met
    210                    215                    220
Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Leu Cys Pro Thr
225                    230                    235                    240
Arg Glu Arg Arg Pro Ala Ser Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                245                    250                    255
Xaa Xaa Lys Val Ser Tyr Ser Gln Ile Trp Glu Ser Val Tyr Ala Arg
            260                    265                    270
Arg Trp Pro Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Asn Tyr Asp Val
        275                    280                    285
Val Ser Thr Leu Pro Gln Val Val Met Gly Ser Ser Tyr Xaa Xaa Xaa
    290                    295                    300
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Phe Gln Tyr Ser Pro Gly Gln
305                    310                    315                    320
Arg Val Glu Phe Leu Val Asn Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                325                    330                    335
Xaa Xaa Xaa Gly Asn Gln Arg Lys Thr Pro Trp Ala Phe His Met Thr
            340                    345                    350
Leu Ala Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg
        355                    360                    365
Leu Asn Gly His Arg Glu Arg His Pro Cys Gly Val Asn Xaa Xaa Xaa
    370                    375                    380
Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Thr Asn Val Val Thr Trp Pro Pro
385                    390                    395                    400
Lys Pro Asp Arg Pro Asn Arg Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa
                405                    410                    415
Xaa His Arg Ala Ala Leu Tyr Arg Gly Ser Ser Asp Phe Lys Arg Arg
        420                    425                    430
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Thr Ala Val Ile Ala
        435                    440                    445
Gly Ala Ala Arg Ala Ala Cys Arg Leu Xaa Xaa Xaa Xaa Xaa Xaa
    450                    455                    460
Xaa Xaa Xaa Xaa Xaa Xaa Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu
465                    470                    475                    480
Lys Ala Ser Ala Ala Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            485                    490                    495
Lys Xaa Xaa Ser Cys Glu Ala Pro Gly Leu His Asp Ala Arg Glu Arg
        500                    505                    510
Arg Arg Gln Glu Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ser
        515                    520                    525
Leu Ser Val Lys Ala Arg Glu Pro Lys Arg Thr Arg Arg Ala Xaa Xaa
    530                    535                    540
Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Leu Arg Val Phe Thr Glu Ala Met
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                         545                          550                          555                          560
                         Thr Arg Tyr Ser Ala Pro Pro Gly Xaa Xaa
                                         565                  570


<210> 4
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<212> PRT
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<220>
<223> DNA encoding fusion protein consisting of a
      portion of HCV polymerase and histidine tag at the
      C-terminus

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1                   5                   10                  15
Ala Glu Glu Ser Lys Leu Pro Ile Asn Ala Leu Ser Asn Ser Leu Leu
                20                  25                  30
Arg His His Asn Met Val Tyr Ala Thr Thr Ser Arg Ser Ala Gly Leu
            35                  40                  45
Arg Gln Lys Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His
        50                  55                  60
Tyr Arg Asp Val Leu Lys Glu Met Lys Ala Lys Ala Ser Thr Val Lys
65                  70                  75                  80
Ala Lys Leu Leu Ser Val Glu Glu Ala Cys Lys Leu Thr Pro Pro His
                85                  90                  95
Ser Ala Lys Ser Lys Phe Gly Tyr Gly Ala Lys Asp Val Arg Asn Leu
            100                 105                 110
Ser Ser Lys Ala Val Asn His Ile His Ser Val Trp Lys Asp Leu Leu
        115                 120                 125
Glu Asp Thr Val Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu
        130                 135                 140
Val Phe Cys Val Gln Pro Glu Lys Gly Gly Arg Lys Pro Ala Arg Leu
145                 150                 155                 160
Ile Val Phe Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu
                165                 170                 175
Tyr Asp Val Val Ser Thr Leu Pro Gln Val Val Met Gly Ser Ser Tyr
                180                 185                 190
Gly Phe Gln Tyr Ser Pro Gly Gln Arg Val Glu Phe Leu Val Asn Thr
        195                 200                 205
Trp Lys Ser Lys Lys Asn Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys
        210                 215                 220
Phe Asp Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile
225                 230                 235                 240
Tyr Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser
                245                 250                 255
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Leu Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly
            260                 265                 270
Gln Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr
            275                 280                 285
Ser Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys
            290                 295                 300
Arg Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Asn Gly Asp Asp
305                 310                 315                 320
Leu Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser
                325                 330                 335
Leu Arg Val Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
                340                 345                 350
Asp Pro Pro Gln Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
                355                 360                 365
Ser Asn Val Ser Val Ala His Asp Ala Ser Gly Lys Arg Val Tyr Tyr
            370                 375                 380
Leu Thr Arg Asp Pro Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr
385                 390                 395                 400
Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr
                405                 410                 415
Ala Pro Thr Leu Trp Ala Arg Met Ile Leu Met Thr His Phe Phe Ser
                420                 425                 430
Ile Leu Leu Ala Gln Glu Gln Leu Glu Lys Ala Leu Asp Cys Gln Ile
            435                 440                 445
Tyr Gly Ala Cys Tyr Ser Ile Glu Pro Leu Asp Leu Pro Gln Ile Ile
            450                 455                 460
Glu Arg Leu His Gly Leu Ser Ala Phe Ser Leu His Ser Tyr Ser Pro
465                 470                 475                 480
Gly Glu Ile Asn Arg Val Ala Ser Cys Leu Arg Lys Leu Gly Val Pro
                485                 490                 495
Pro Leu Arg Val Trp Arg His Arg Ala Arg Ser Val Arg Ala Arg Leu
                500                 505                 510
Leu Ser Gln Gly Gly Arg Ala Ala Thr Cys Gly Lys Tyr Leu Phe Asn
            515                 520                 525
Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Ile Pro Ala Ala Ser
            530                 535                 540
Gln Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Ser Gly Gly Asp
545                 550                 555                 560
Ile Tyr His Ser Leu Ser Arg Ala Arg Pro Arg Gly Ser His His His
                565                 570                 575
His His His
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<210> 5
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<212> DNA
<213> Artificial Sequence

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<220>
<221> primer_bind
<222> (1)...(30)
<223> Artificially synthesized primer sequence, 5BNde1FW

<223> DNA encoding fusion protein consisting of a
      portion of HCV polymerase and histidine tag at the
      C-terminus

<400> 5
catatgtcaa tgtcctacac atggacagcc                                        30


<210> 6
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(57)
<223> Artificially synthesized primer sequence, 5B570HRV

<223> DNA encoding fusion protein consisting of a
      portion of HCV polymerase and histidine tag at the
      C-terminus

<400> 6
ttattagtga tggtgatggt gatgggatcc gcggggtcgg gcacgagaca ggctgtg      57


<210> 7
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(57)
<223> Artificially synthesized primer sequence, 5B552HRV

<223> DNA encoding fusion protein consisting of a
      portion of HCV polymerase and histidine tag at the
      C-terminus

<400> 7
ttattagtga tggtgatggt gatgggatcc aacgaaccag ccggacaagt ccagctg      57


<210> 8
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<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(57)
<223> Artificially synthesized primer sequence, 5B544HRV

<223> DNA encoding fusion protein consisting of a
       portion of HCV polymerase and histidine tag at the
       C-terminus

<400> 8
ttattagtga tggtgatggt gatgggatcc ctgggacgca gccgggattg gagtgag   57

<210> 9
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(67)
<223> Artificially synthesized primer sequence,
       5B536HRV

<223> Artificially synthesized primer sequence 5B531HRV

<400> 9
ttattagtga tggtgatggt gatgggatcc gagtttgagt ttggtcttca ctgcccagtt 60
gaagagg   67

<210> 10
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(60)
<223> Artificially synthesized primer sequence,
       5B531HRV

<223> Artificially synthesized primer sequence 5B591HRV

<400> 10
ttattagtga tggtgatggt gatgggatcc cttcactgcc cagttgaaga ggtacttgcc 60

<210> 11
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(52)
<223> Artificially synthesized primer sequence,
       5B591HRV

<223> Artificially synthesized primer sequence

<400> 11
ttattaatgg tgatggtgat ggtgtccgga tcgattgggg agcaggtaga tg   52

<210> 12
<211> 8
<212> PRT
<213> Hepatitis C Virus

<220>
<221> VARIANT
<222> 1, 8
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 1, 8
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 1, 8
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 1, 8
<223> Xaa = Any Amino Acid

<400> 12
Xaa Asp Leu Ser Gly Trp Phe Xaa
 1   5

<210> 13
<211> 8
<212> PRT

<213> Hepatitis C Virus

<400> 13
Lys Asp Leu Ser Gly Trp Phe Lys
 1   5